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Coprinellus ovatus sp. nov. from Pakistan

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Abstract—A *Coprinellus* specimen collected in Islamabad, Pakistan, showed characters that were distinct from those of all other *Coprinellus* spp.: an ovoid shaped pileus; a caespitose stipe base; utriform cheilocystidia bearing crystals; a pileipellis of loosely arranged clavate to mucronate hyphae; and basidiospores (9.5–11.6 × 6.0–7.8 × 5.6–6.2 µm) with shapes ranging from mitriform or triangular to ellipsoid in face view, amygdaliform to ellipsoid in side view. Combination of all these characters and molecular analysis of ITS sequences support its identification as a new species.

Key words—coprinoid mushrooms, *Micacei*, *Psathyrellaceae*, taxonomy

Introduction

Coprinoid mushrooms are an important group of macrofungi that can be readily distinguished from normal agarics by having gills that liquify at maturity. As a result, coprinoid mushrooms are often called inky caps. Coprinoid mushrooms, which are characterized by thin fragile pilei that become plicate on opening, deliquescent gills, and dark brown to blackish basidiospores with germ-pores (Schafer 2014), spread across *Agaricales* in evolutionary lineages that are either fully or partially coprinoid (Tóth & al. 2013). Fully coprinoid genera include: *Coprinus* Pers., *Coprinellus* P. Karst., *Coprinopsis* P. Karst., and *Parasola* Redhead & al. Some species of *Leucocoprinus* Pat., *Conocybe* Fayod, *Bolbitius* Fr., and *Galerella* Earle show coprinoid combinations of characters (Matheny & al. 2006, Nagy 2011, Nagy & al. 2011, Tóth & al. 2013).

Coprinellus, with approximately 84 described species, represents an independent lineage in *Psathyrellaceae* (Redhead & al. 2001; Walther & al. 2005; Padamsee & al. 2008; Vašutová & al. 2008; Nagy & al. 2011, 2012, 2013; Örstadius & al. 2015; Hussain & al. 2018a). These mushrooms are commonly found on bare soil, wood chips, grassy debris, leaf-litter, and herbivore dung (Schafer 2010). *Coprinellus* species are divided into three sections based on veil anatomy and the presence or absence of cap pileocystidia. *Coprinellus* sect. *Domestici* (Singer) D.J. Schaf. is characterized by a pileus veil comprising floccose scales consisting of chains of fusiform or subglobose cells, often with encrusted walls. In *C.* sect. *Micacei* (Fr.) D.J. Schaf., veil remnants are present in the form of scattered (often disappearing) granulose flocks of globose cells arising from a matrix of narrow branched hyphae. In *C.* sect. *Setulosi* (J.E. Lange) D.J. Schaf., the veil may be present or absent, but the pileus and stipe are covered with thin-walled pileocystidia and caulocystidia, respectively (Schafer 2010). However, Nagy & al. (2012) showed that molecular phylogeny did not entirely support these sections in that clades corresponding to *C.* sect. *Micacei* and *C.* sect. *Domestici* each included some setulose species.

Twenty-two coprinoid species have been reported from Pakistan (Ahmad & al. 1997; Hussain & al. 2016, 2017, 2018a,b), of which eight belong to *Coprinellus: C. campanulatus* S. Hussain & H. Ahmad, *C. disseminatus* (Pers.) J.E. Lange, *C. disseminatisimilis* S. Hussain, *C. marculentus* (Britzelm.) Redhead & al., *C. micaceus* (Bull.) Vilgalys & al., *C. pakistanicus* Usman & Khalid, *C. radians* (Desm.) Vilgalys & al. *C. tenuis* S. Hussain (Ahmad & al. 1997; Hussain & al. 2018b).

During surveys of basidiomycetous fungi of Pakistan in 2018, one interesting collection presenting a *Coprinellus* morphology was encountered. Closer inspection revealed that this collection presented a unique combination of features compared with other *Coprinellus* species. Here we propose a new species based on morphological characters and molecular phylogenetic analysis of rDNA internal transcribed spacer (ITS).

Materials & methods

The sample was collected from the capital territory Islamabad, Pakistan, along the Murree Express Road. Islamabad (33.43°N 73.04°E) lies at the edge of the Pothohar Plateau at the base of the Margalla Hills, occupies an area of 906 km^2 with elevation of 507 m a.s.l., and has a humid subtropical climate (Köppen climate classification). The territory recognizes winter (November–February), spring (March–April), summer (May–June), rainy monsoon (July–August), and autumn (September–October), with June the hottest month with the average temperature routinely exceeding 38°C

Table 1. *Coprinellus* and *Psathyrella* species and specimens used for the molecular phylogenetic analysis.

Species	Voucher	Country	ITS #
C. aff. *eurysporus* (as *C.* sp. in GenBank)	NL-3418	Hungary	JN159540
C. aff. *xanthothrix* (as *C. xanthothrix* in GenBank)	NL-1292	Sweden	FM878008
C. angulatus	NL-1934	Hungary	HQ846994
	Arnolds99-22	Netherlands	JN159536
	NL-0906	Hungary	JN159535
C. bisporiger	WU7403	Hungary	HQ846974
	Daams71-98	Hungary	JN159520
C. bisporus	NL-0158	Sweden	GU227705
	NL-2512	Sweden	FN396107
	WU6011	Sweden	JN159517
C. brevisetulosus	NL-1445	Hungary	GU227710
C. callinus	NL-1931	Hungary	FN396105
	Ulje1204	Netherlands	JN159518
C. campanulatus	Coprinellus _sp._SHP144	Pakistan	MH753666
	Coprinellus _sp._SH144T	Pakistan	MH753667
C. cinereopallidus	NL-0177	Hungary	HQ847001
	Ulje1163	Netherlands	JN159524
C. congregates	NL-0588	Sweden	FM878013
	NL-2138	Hungary	JN159554
	NL-1221	Hungary	JN159550
	NL-1433	Hungary	JN159552
C. curtus	NL-1490	Hungary	JN159569
	NL-2339	Sweden	FM878016
	NL-1023	Hungary	JN159568
C. deminutus	NL-0761	Hungary	JN159572
C. disseminatisimilis	Coprinellus _sp._SH15	Pakistan	MH753668
	Coprinellus _sp._Cr_3wT	Pakistan	MH753670
	Coprinellus _sp._Cr_3b	Pakistan	MH753669
C. disseminates	NL-2337	Sweden	FM878017
	NL-0786	Hungary	JN159560
	NL-3401	Hungary	JN159561
C. domesticus	Cervenka286	Hungary	HQ847043
	TOK21808	Netherlands	JN159580
C. eurysporus	NL-1761	Hungary	HQ846992
C. flocculosus	NL-0838	Hungary	JN159573
	NL-1567	Hungary	JN159575
	NL-1661	Norway	FN396138
C. flocculosus (as *Coprinus* "*maysoidisporus*")	FVDB1743	Hungary	JN159574
C. fuscocystidiatus	NL-2720	Norway	HQ846977
	NL-3622	Sweden	JN159514
C. hiascens	NL-1349	Hungary	JN159525
	NL-2536	Norway	FM878018
	NL-1350	Hungary	GU227720
	NL-2598	Hungary	JN159526
C. impatiens	NL-1164	Hungary	FM163177
	NL-0568	Hungary	JN159511

Table 1, continued on p. 324

Table 1, continued

Species	Voucher	Country	ITS #
C. micaceus	NL-3888	Hungary	GU227721
	NL-3656	Hungary	JN159567
	NL-1939	Hungary	FN396104
	NL-4253	Hungary	JN159566
	NL-2739	Hungary	JN159564
	NL-2744	Hungary	JN159565
[as *C.* sp. 10 LGN-2011 in GenBank & *C. "xylophilus"* in Nagy & al. 2011]	FVBD1726	Hungary	JN159563
C. ovatus	**LAH35939**	**Pakistan**	**MK764023**
C. pakistanicus	LAH35322	Pakistan	MH366735
	LAH35323	Pakistan	MH366736
	LAH35324	Pakistan	MH366737
C. pallidus	NL-1556	Hungary	JN159521
	NL-0625	Hungary	HQ846989
	NL-4218	Hungary	JN159522
C. pellucidus	NL-1076	Hungary	GU227713
	NL-2928	Slovakia	GU227714
	NL-2344	Hungary	FM878023
C. plagioporus	NL-1365	Hungary	HQ846981
	NL-1086	Hungary	JN159512
C. radians	NL-1373	Sweden	JN159579
	NL-3896	Sweden	HQ847045
C. radicellus	NL-3168	Sweden	GU227719
	NL-0594	Sweden	GU227716
	NL-0957	Norway	GU227718
	NL-2121	Sweden	GU227717
Coprinellus sabulicola	NL-1560	Hungary	JN159557
	NL-2906	Hungary	JN159558
	NL-1027	Hungary	JN159559
	NL-1763	Hungary	HQ847007
C. sassii	NL-1495	Hungary	FN396101
	NL-1237	Hungary	JN159509
C. sclerocystidiosus	NL-0797	Hungary	JN159539
	NL-1022	Hungary	JN159538
	NL-1761	Hungary	HQ846992
	NL-1444	Hungary	JN159537
C. silvaticus	NL-3035	Hungary	HQ846986
C. subimpatiens	ToK 27/8-08	Hungary	HQ846993
	NL-0162	Hungary	JN159542
	Uljé 1191	Netherlands	HQ846995
C. tenuis	Coprinellus _sp._SHP10	Pakistan	MH753663
	Coprinellus _sp_SH10T	Pakistan	MH753664
C. truncorum	NL-1101	Hungary	JN159562
	NL-1294	Sweden	FM878007
C. uljei	NL-2492	Sweden	JN159513
	NL-0157	Sweden	HQ846982
	NL-3985	Slovakia	JN159515
C. verrucispermus	NL-2146	Hungary	JN159577
C. xanthothrix	TOK12808	Netherlands	JN159578
	NL-3417	Hungary	HQ847044
Psathyrella candolleana	NFP-MU1	India	KT443864

* Species information in bold face represents data generated during this study.

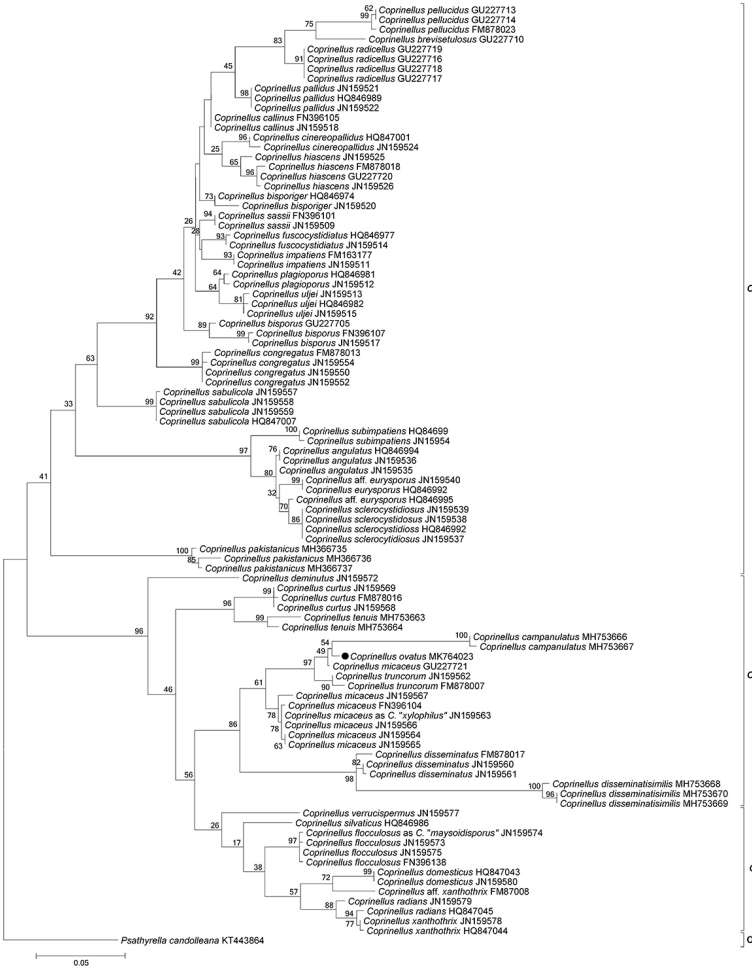

FIGURE. 1. Molecular phylogenetic analysis of *Coprinellus* spp. based in ITS sequences. The tree with the highest log likelihood (–5095.2205) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial trees for the heuristic search were obtained by applying the Neighbor-Joining method to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories; +G, parameter = 0.2939). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 96 nucleotide sequences. The sequence generated from LAH35939 is marked with●.

and July the wettest (https://en.wikipedia.org/wiki/Climate_of_Islamabad; Peel & al. 2007, Belda & al. 2014).

Basidiomata were tagged, photographed, and dried. Morphological features (size, shape, and color) of basidiomata were noted in the field. Color was coded following Munsell (1975). Tissues were mounted in 2% aqueous KOH (w/v) solution for anatomical study and examined using a China XSZ-107-BN light microscope. At least 20 measurements were recorded for each anatomical feature. Basidiospore measurements were taken as: length range × width range × breadth range, with outliers shown in parentheses; Q values designate length/width ratios, with Qav = the average Q value. The specimens are deposited at the Herbarium, Department of Botany, University of the Punjab, Lahore, Pakistan (LAH).

DNA was extracted using Extract-N-Amp™ Plant Tissue PCR Kit following manufacturer's instructions. PCR amplification and sequencing were commercially performed by TsingKe, P.R. China.

For phylogenetic analysis, the ITS sequences generated from the Pakistani collections were compared with other sequences in GenBank using Basic Local Alignment Search Tool (BLAST) at NCBI (https://www.ncbi.nlm.nih.gov/). Closely matching sequences and those cited in Hussain & al. (2018b) were downloaded from the GenBank for phylogenetic analysis. *Psathyrella candolleana* (Fr.) Maire (HQ847040) was chosen as an outgroup (Hussain & al. 2018b). Sequences were aligned using online MUSCLE tool (http://www.ebi.ac.uk/). Best model selection approach was employed on the final data set and Maximum Likelihood (ML) analysis was performed by using Tamura-Nei model (Tamura & Nei 1993) in MEGA 6 (Tamura & al. 2013). The phylogenetic tree was constructed at one thousand rapid bootstrap replicates.

Molecular phylogenetic results

The sequences from specimens used for the molecular phylogenetic analysis are given Table 1. The final ITS dataset comprised 96 nucleotide sequences, with 697 positions after trimming from both ends. The resultant phylogenetic tree (Figure 1) places the *Coprinellus* sequences in several distinct clades that more or less correspond to previous studies (Nagy & al. 2012, Hussain & al. 2018b). The sequence generated from LAH35939 clustered in *C.* sect. *Micacei*.

Taxonomy

Coprinellus ovatus Kamran & Jabeen, **sp. nov.** Figures 2, 3

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Differs from *Coprinellus campanulatus* by its ovate fibrillose pileus, brownish black hymenium, caespitose stipe base, larger mitriform, amygdaliform, and ellipsoid basidiospores, crystal-bearing utriform cheilocystidia, and loosely arranged clavate to mucronate pileipellis hyphae.

Figure. 2. *Coprinellus ovatus* (holotype, LAH35939). Basidiomata.
Scale bars: A = 1 cm; B, C = 0.2 cm. Photographs by Muhammad Kamran.

Type: Pakistan, Islamabad, on soil under broadleaf trees, 1 May 2018, Muhammad Kamran K4 (LAH35939).

Etymology: The specific epithet (L.) refers to oval shape of the pileus.

Pileus 9–13 × 14–17 mm, ovoid to parabolic, with plane center, orange yellow color (10YR8/8), surface fibrillose, deeply plicate from center to margin. Lamellae 1.5–2.5 mm wide, free, entire, crowded, brownish black (10YR2/3). Lamellulae absent. Stipe 1.4–2.7 × 2–4 mm, central, smooth radicating, base 3–5 mm wide, yellowish brown (10YR7/8), caespitose, dry, fibrillose. Annulus absent. Odor not observed.

Basidiospores (8.6–)9.6–11.4(–11.6) × (5.7–)6.0–7.5(–7.8) × (5–)5.6–6.(–7.2) µm, average = 10.5 × 6.7 × 6.0 µm, Qav = 1.5, mitriform or triangular to ellipsoid in face view, amygdaliform to ellipsoid in side view, dark brown to blackish brown in KOH, apiculus prominent, with central germ-pore (2.2–3.0 µm). Basidia (17.3–)21.8–36.9(–41.7) × (7–)8.25–10.6(–11) µm, cylindrical, clavate to subclavate, hyaline. Cheilocystidia 20–29.3 × 9.2–12.1 µm, utriform, and apex usually bears crystals. Pleurocystidia absent. Pileipellis an epithelium of loosely arranged hyphae with clavate to mucronate terminals (51–)55.5–68(–94) × (14–)20–28(–67) µm. Universal veil elements 19.4–44.2 µm wide, globose to subglobose with filament 9.4–26.2 µm. Stipitipellis (3.2–)11.9–22.9(–29.5) µm, filamentous with frequent septa, with rare clamp connections.

Ecology & distribution—Among broadleaf trees including *Morus* sp.

Discussion

Coprinellus ovatus is phylogenetically most closely related to *C. campanulatus* and *C. truncorum*. *Coprinellus campanulatus* is separated morphologically by a campanulate pileus, pale orange-yellow to dark yellowish-brown lamellae, the presence of lamellulae, smaller basidiospores, larger cheilocystidia, and a pileipellis that is an epithelium of loosely arranged globose to subglobose pileocystidia (Hussain & al. 2018b). *Coprinellus truncorum* differs in the presence of lamellulae and smaller ellipsoid basidiospores that are not distinctly lentiform (Keirle & al. 2004, Uljé 2005).

Coprinellus micaceus differs in its closely crowded adnexed to free lamellae and smaller basidiospores that are lacriform to submitriform or mitriform in face view, and conical towards the base (Keirle & al. 2004, Uljé 2005).

Coprinellus ovatus also differs from three recently described species from Pakistan. *Coprinellus disseminatisimilis* is diagnosed by its pruinose parabolic to umbo-campanulate pileus, sinuate to uncinate lamellae, the presence of lamellulae, ellipsoid to cylindrical/obovoid basidiospores, much larger narrowly clavate to utriform cheilocystidia, and a loosely arranged euhymeniderm pileipellis with more or less utriform pileocystidia (Hussain

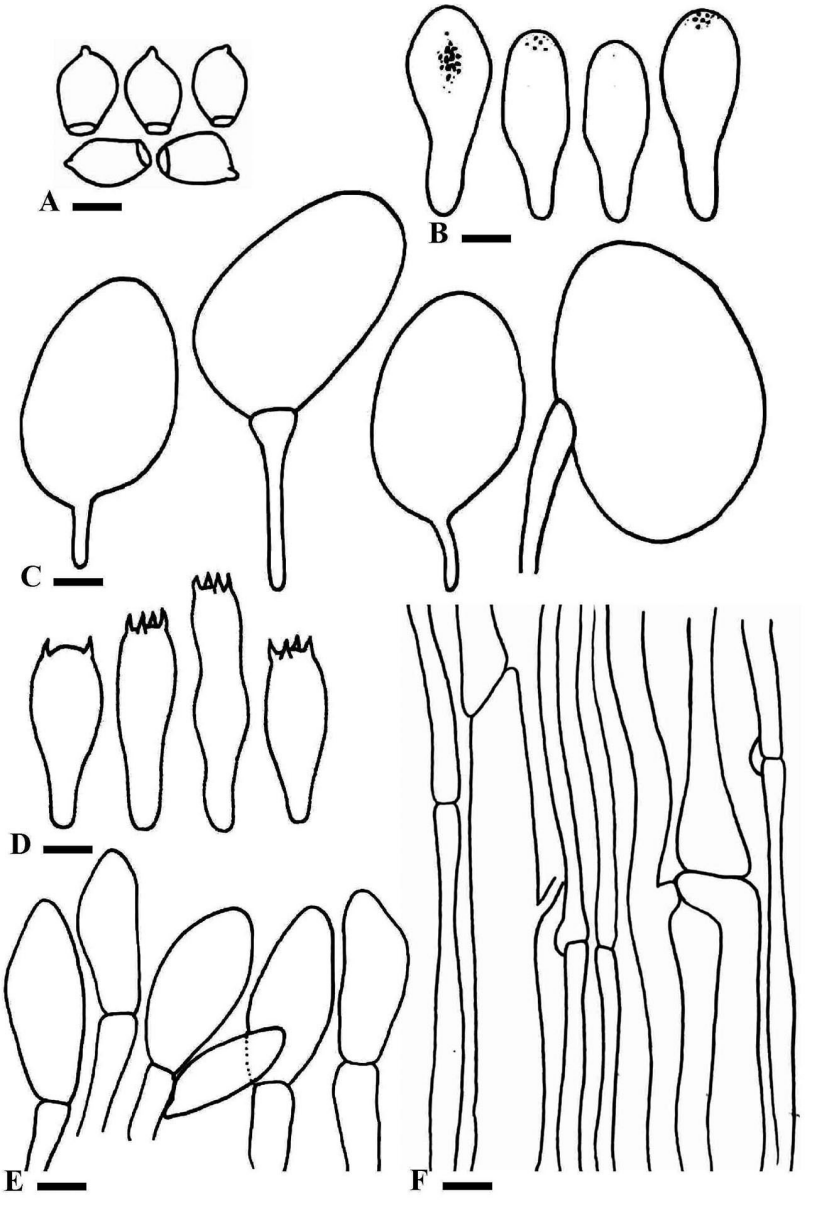

Figure. 3. *Coprinellus ovatus* (holotype, LAH35939). A. Basidiospores; B. Cheilocystidia; C. Universal veil elements; D. Basidia; E. Pileipellis hyphae with clavate to mucronate terminals; F. Stipitipellis. Scale bars: A–D = 6 µm; E, F = 15 µm. Drawing by Sana Jabeen.

& al. 2018b). *Coprinellus pakistanicus* differs by its convex to plane pileus, the presence of lamellulae, slightly smaller basidiospores, larger cheilocystidia; and the presence of true lageniform/cylindrical pileocystidia (Hussain & al. 2018b). *Coprinellus tenuis,* which produces similar basidiospores, is separated by its convex to plane pileus, sinuate to uncinate lamellae, presence of lamellulae, equal cylindrical stipe, and the presence of lageniform to cylindrical pileocystidia (Hussain & al. 2018b).

Table 2. Comparison of *Coprinellus ovatus* and related species.

Coprinellus sp.	Pileus (mm); Shape; Surface	Lamellar attachment (lamellulae)	Basidiospores (µm) F = face view S = side view	Pileipellis type (terminal cells)	Cheilocystidia (µm)
ovatus	9–13 × 14–17; Ovoid to parabolic; Fibrillose	Free, (absent)	9.6–11.4 × 6–7.5 F: mitriform / ellipsoid; S: amygdaliform / ellipsoid	Loose epithelium (clavate / mucronate)	20–29.3 × 9.2–12.1
campanulatus	≤40 × 15 Yg: ovoid / parabolic, later campanulate; Pruinose to granulose	Adnexed, (present, 1–4 series)	8–10.5 × 5.5–6.5 F: mitriform / ellipsoid; S: cylindrical, amygdaliform / ellipsoid	Loose epithelium (globose to subglobose elements)	36–47 × 35–45
disseminati-similis	≤20 × 20; Parabolic then campanulate; Pruinose to pulverulent	Sinuate to uncinate, (present, 0–2 series)	8–9 × 5–5.5 F: ellipsoid to cylindrical; S: amygdaliform / ellipsoid	Loose euhymeniderm; (utriform pileocystidia)	70–165 × 11–15
micaceus	*≤24 mm diam; Obtuse cylindrical, then convex / campanulate; white mica-like; granular, detersile	Adnexed or free (absent)	6.5–10 × 4.5–7 F: lacriform to mitriform; conical towards the base	* Epithelium (globose cells)	* 30–40 × 20–25
pakistanicus	≤35 mm; Convex to plane, disc depressed; Smooth, pulverulent, granulose	Free (present, 0–2 series)	8.5–11.5 × 6.5–8; F: obovoid to phaseoliform; S: ellipsoid to obovoid	Irregular epithelium (lageniform to cylindrical; tapering neck, obtuse apex)	42–75 × 14–25
tenuis	≤20 mm; Pulvinate, convex, plane; Glabrous, furred	Sinuate to uncinate (present, 0–2 series)	10.5–14.5 × 8–9.5; F: ellipsoid to ovoid S: sl. pyriform to ellipsoid	Loose epithelium (lageniform to obtuse long cylindrical)	22–30 × 19–28
truncorum	* ≤14 mm; Oval then convex; finely plicate, granular or with mica-like flecks	* Adnexed or free (present, 1–4 series)	8.5–9 × 5.5–6; Ellipsoid in all views, not truly lentiform	* Loose epithelium ([sub]globose to broadly clavate)	* 25–40 × 25–30

* Reference for *C. micaceus* and *C. truncorum:* Keirle & al. 2004

Full dimensions and comparative characters of the *Coprinellus* species cited above are given in Table 2. Although *C. ovatus* is in *C.* sect. *Micacei*, it is sister to *C. micaceus* and forms a subclade with *C. truncorum* and *C. campanulatus*. *Coprinellus micaceus* sequence (GU227721) from Hungarian collection (NL-3888) also clustered in the same clade with *C. ovatus*, this specimen showed 99.2% sequence similarity and 0.6% divergence from *C. ovatus*. No morphological data is available from this specimen. Since *C. ovatus* showed remarkable morphological differences from *C. micaceus* (Keirle & al. 2004, Uljé 2005), we conclude that LAH35939 represents a new species in *C.* sect. *Micacei*.

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